

Figure 1

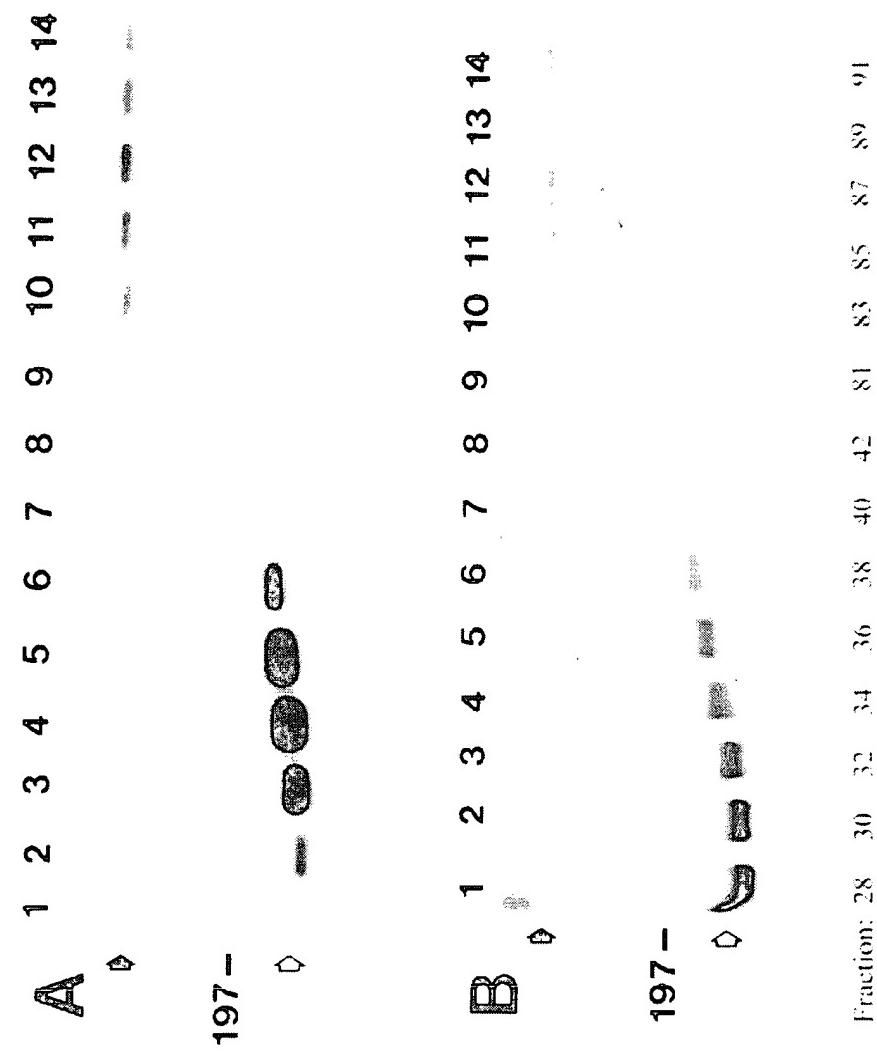
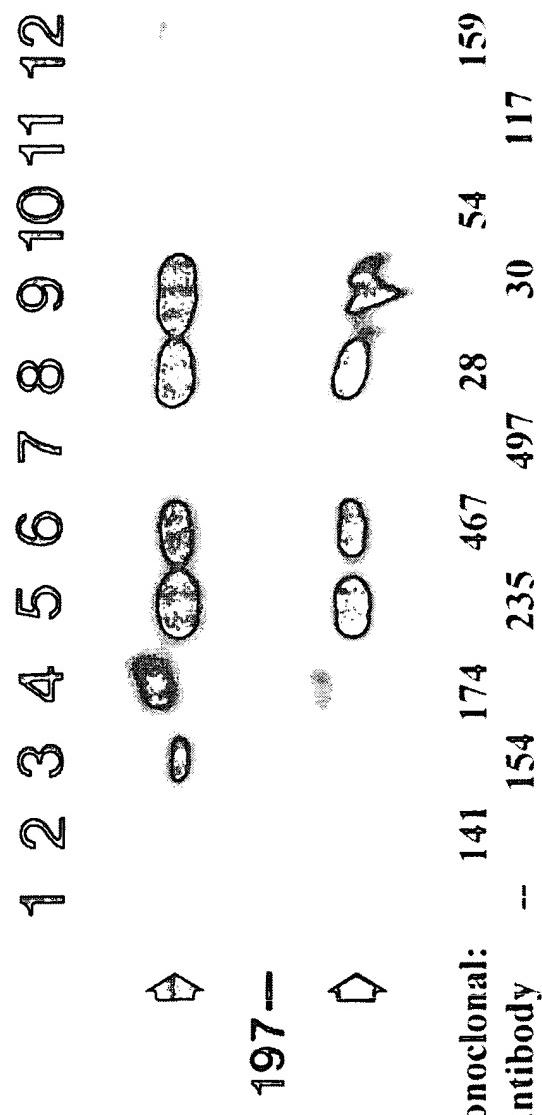


Figure 2



Zhou et al. - Figure 3

Figure 3

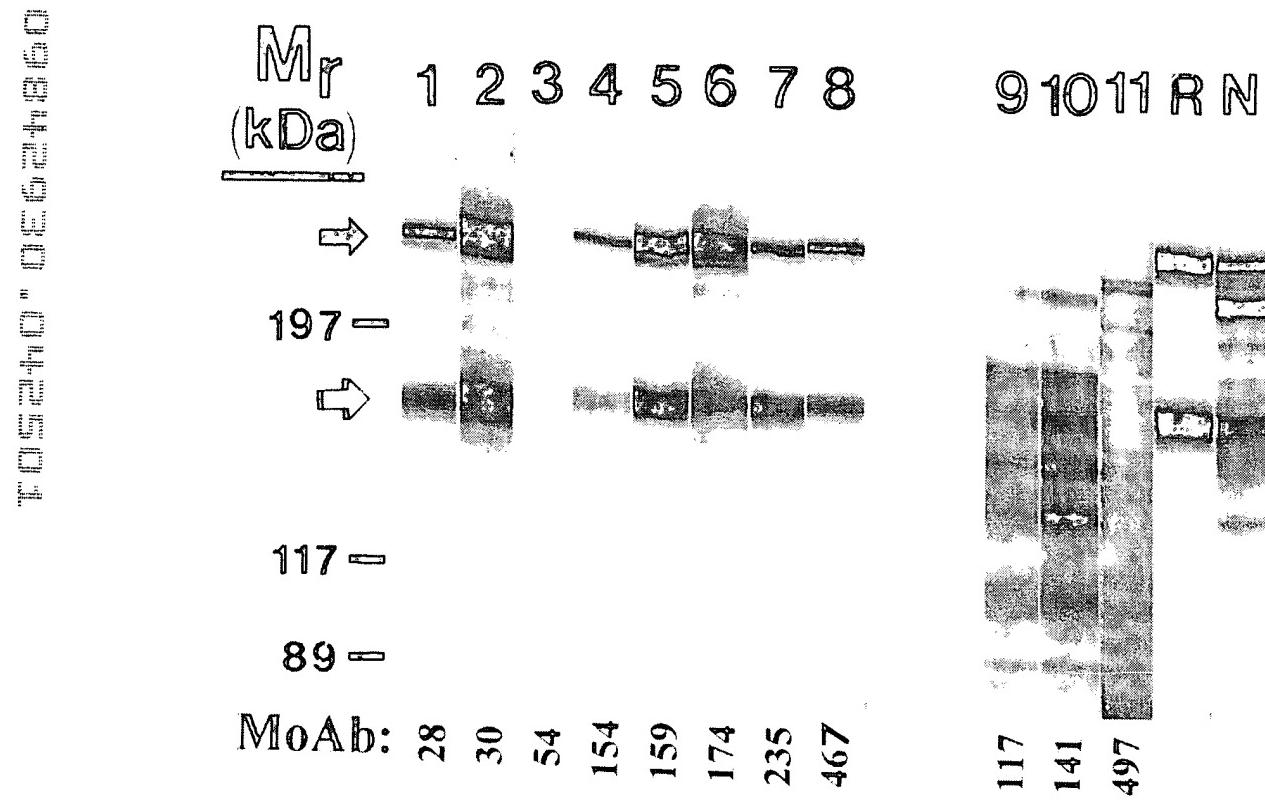
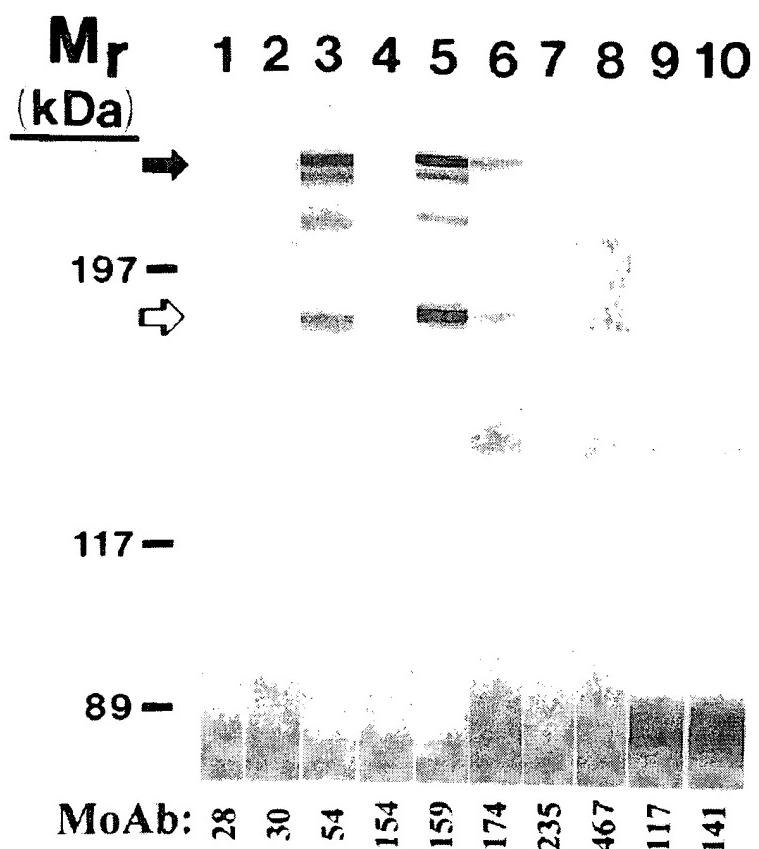
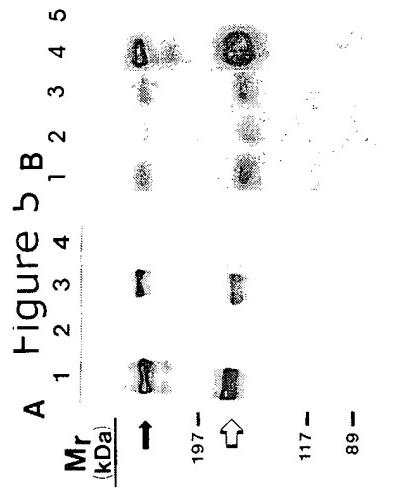


Figure 4





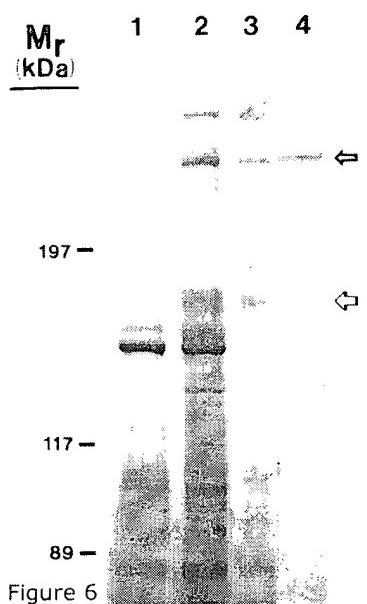
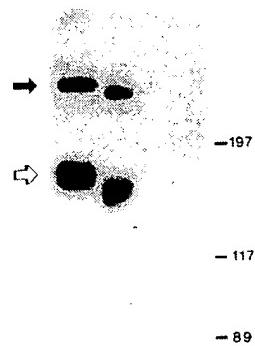


Figure 6

Figure 7 1 2 3 4



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Figure 8A

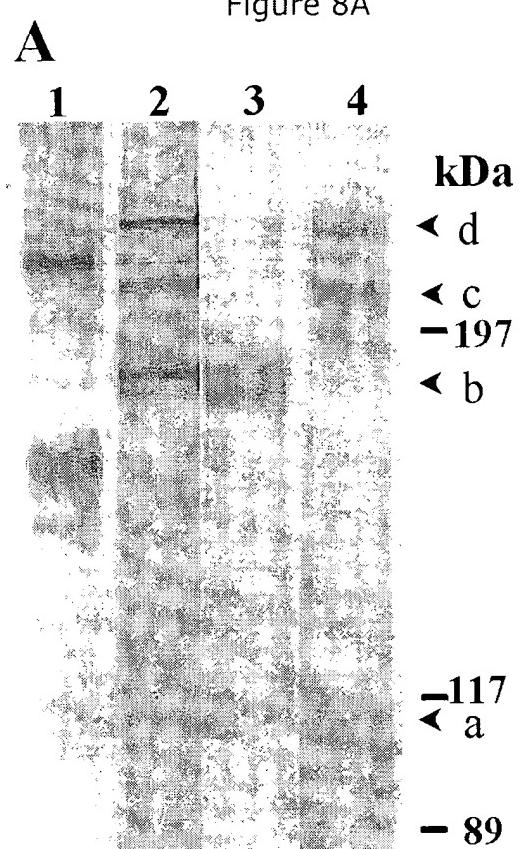
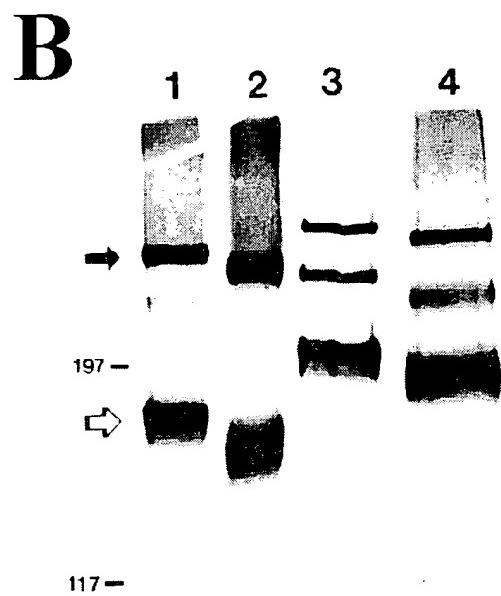
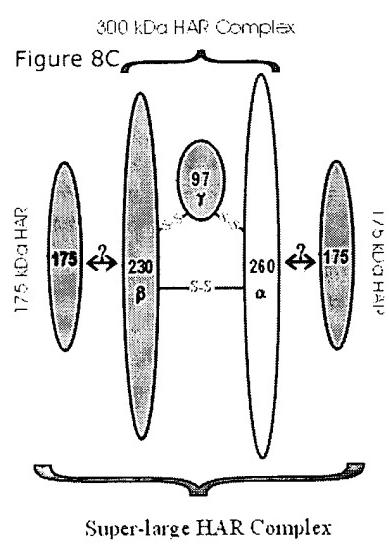


Figure 8B



89—

| | | | | |
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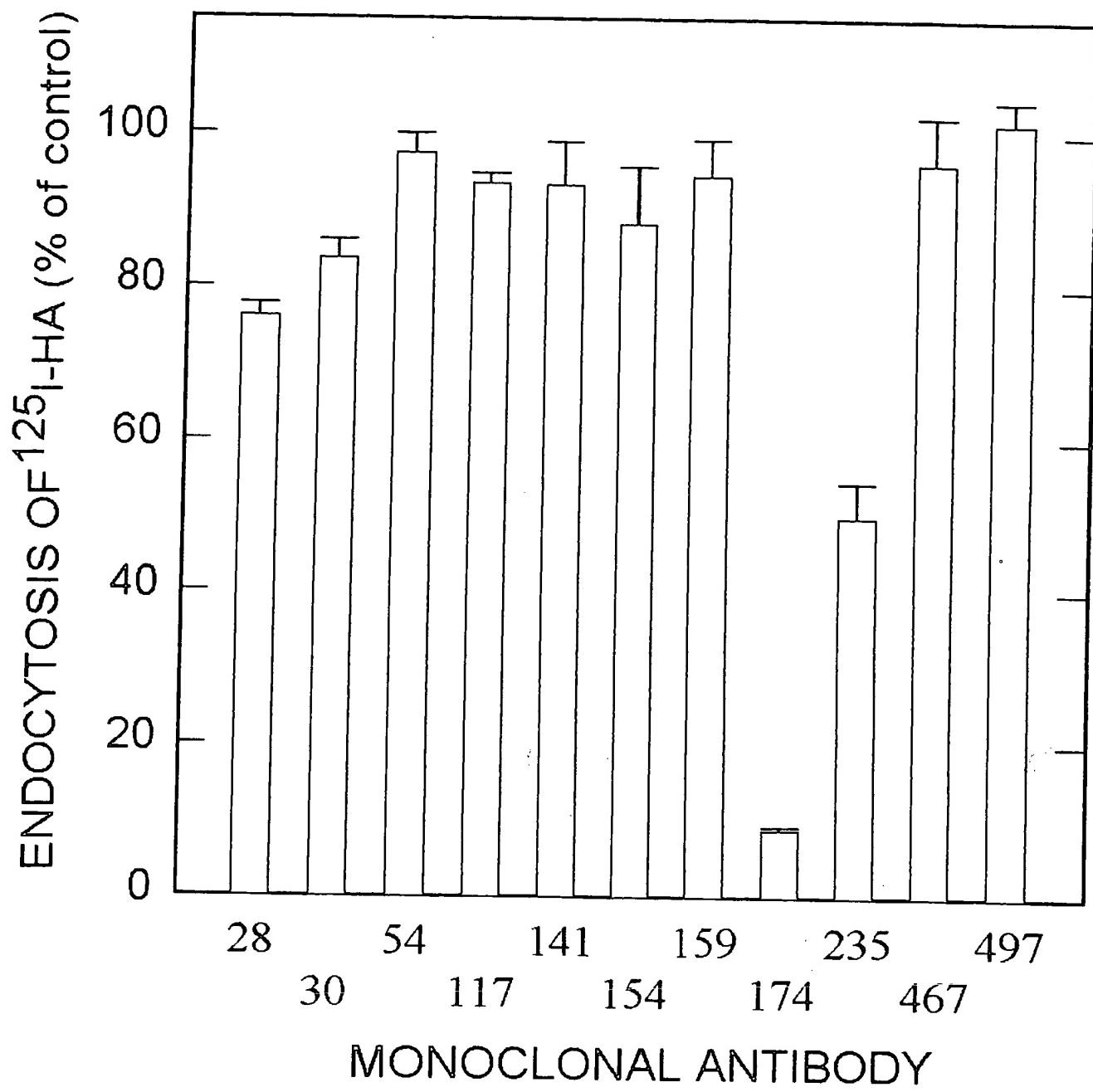
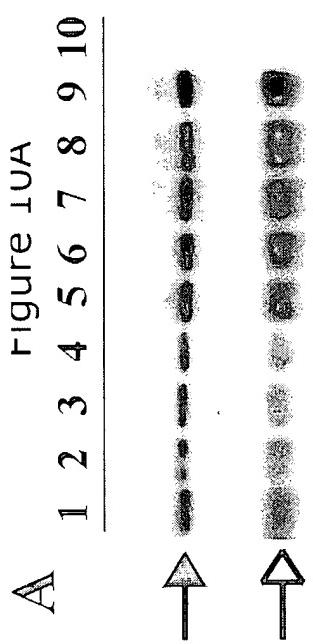


Figure 9



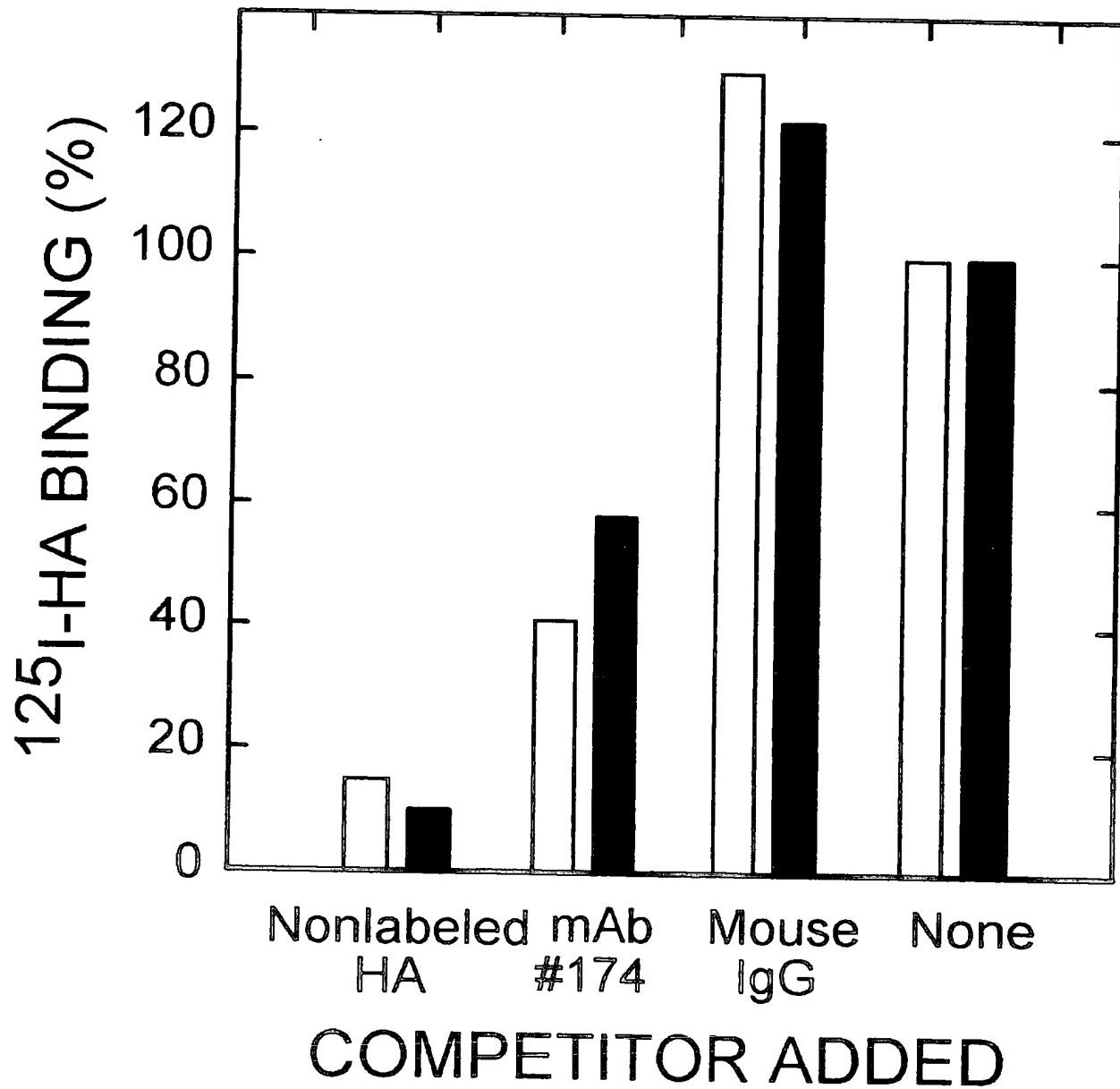


Figure 10B

Figure 11

Antibody Inhibition of HA
Endocytosis by HARE in LECs

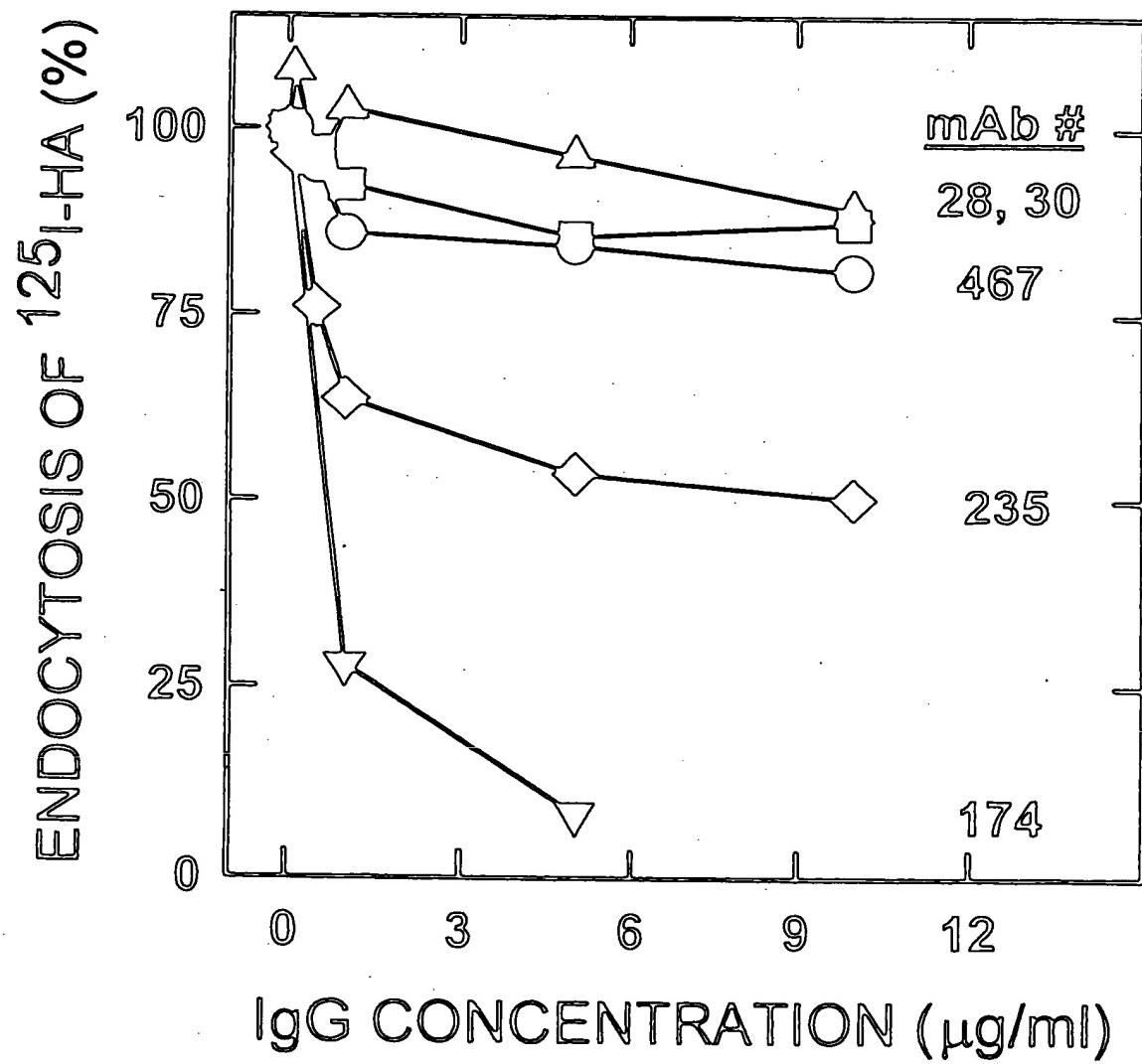


Figure 12

**Antibody Inhibition of HA Binding to HARE
on LECs is Temperature Dependent**

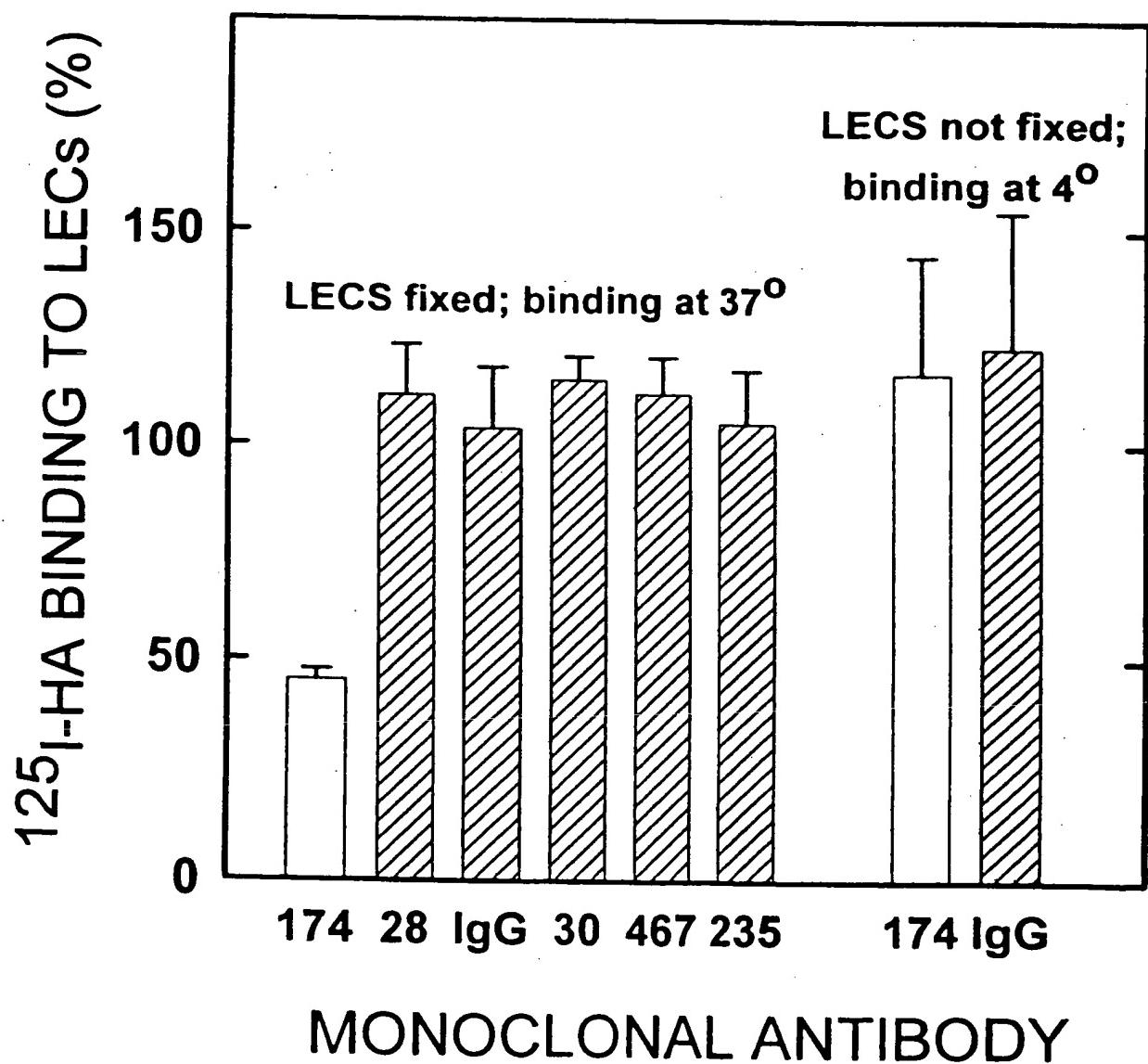
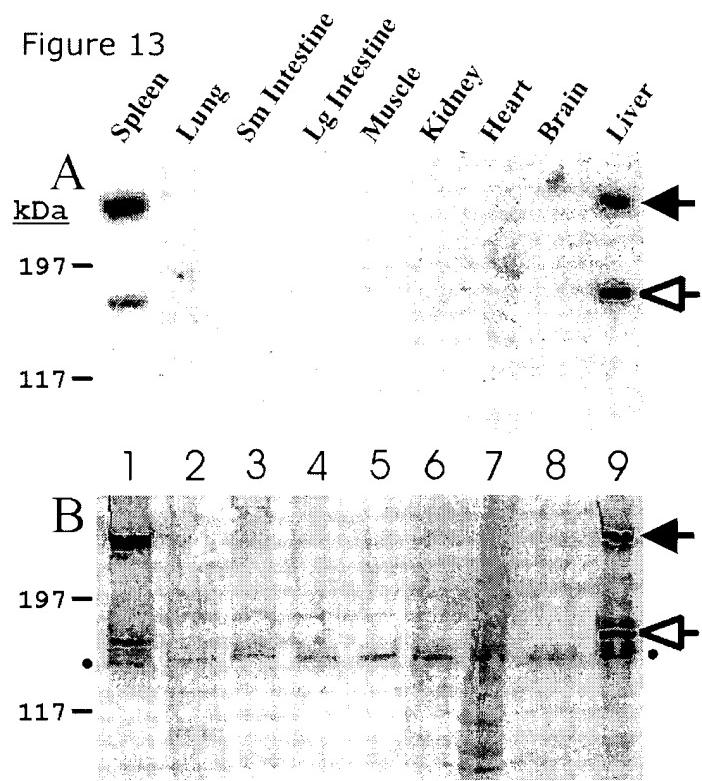


Figure 13



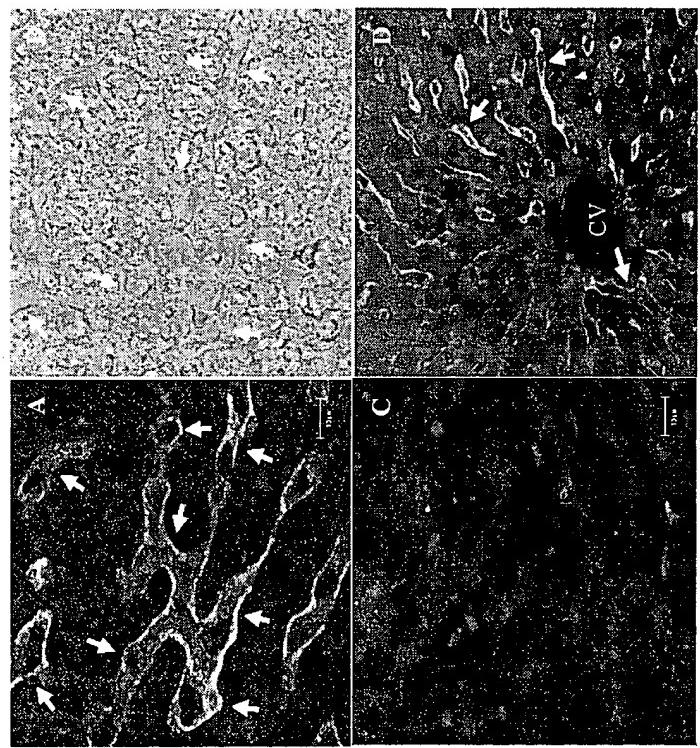
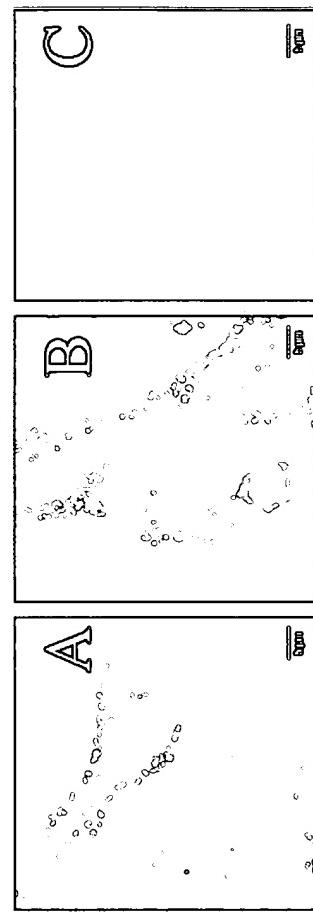


Figure 14

Figure 15



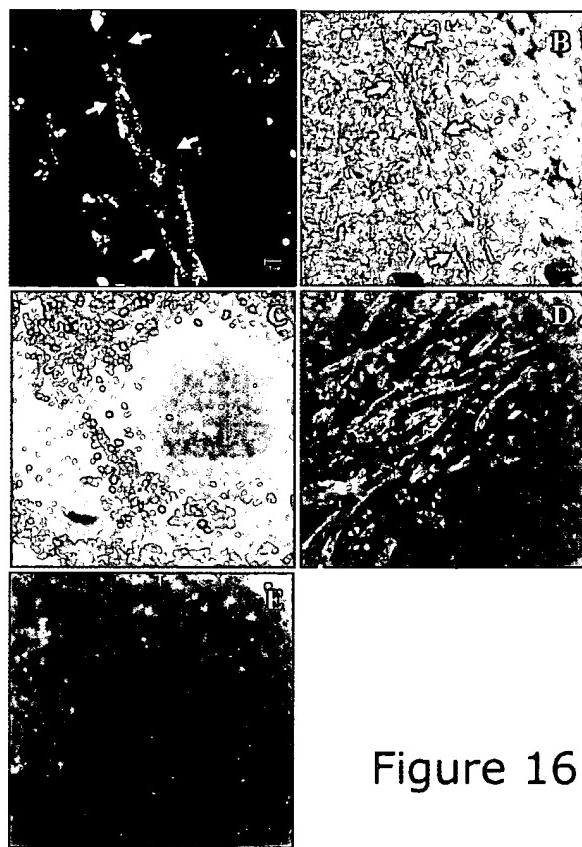


Figure 16

Figure 17

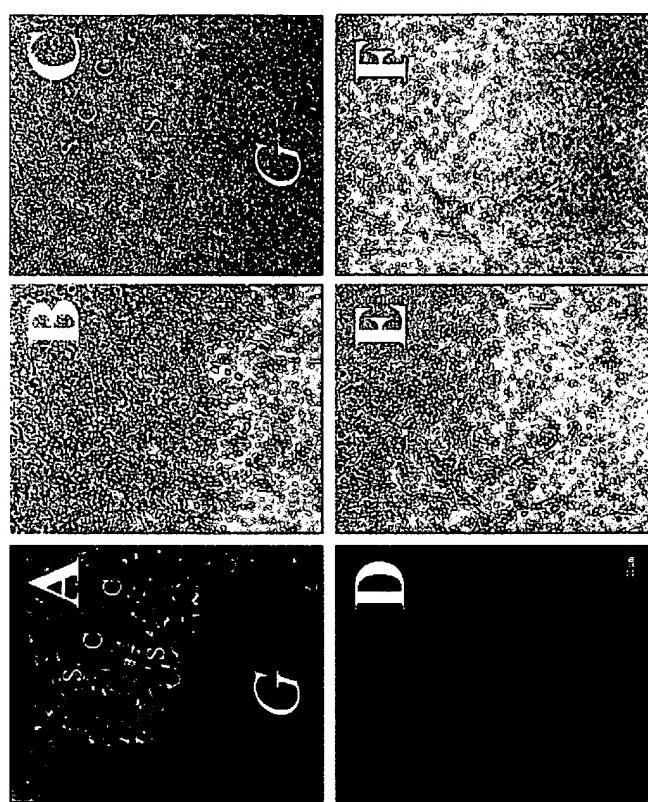
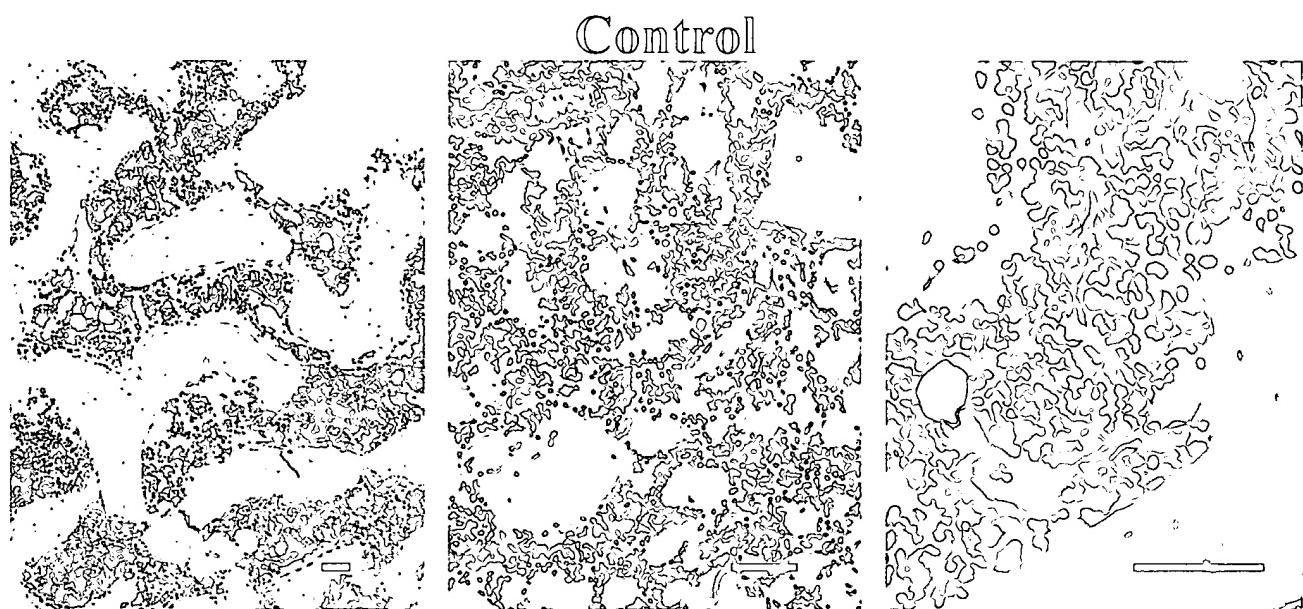


Figure 18

Immunolocalization of HARE
in Bone Marrow



Bars = 50 μm

Figure 19

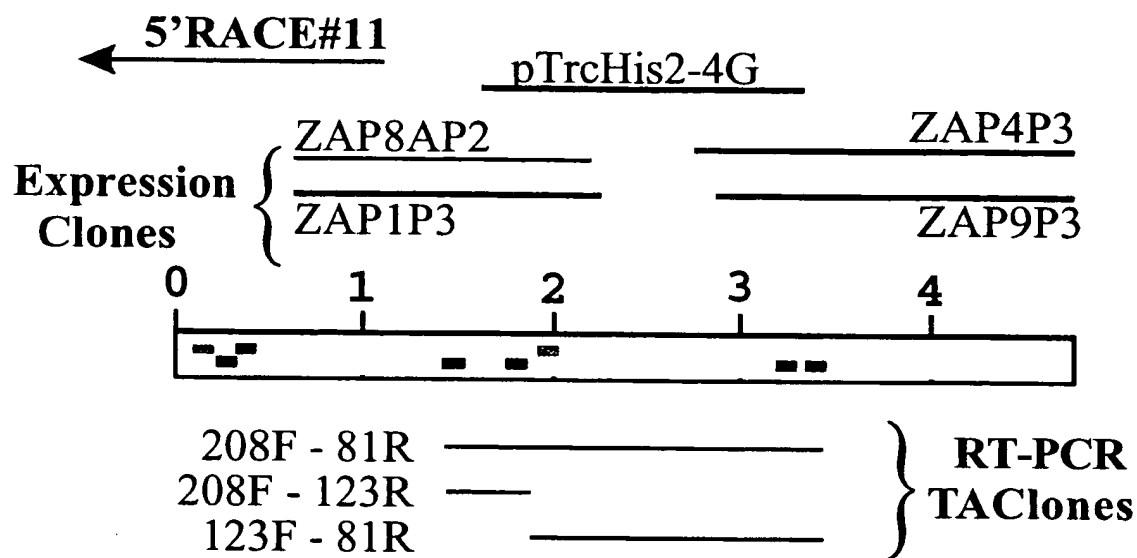


Figure 20

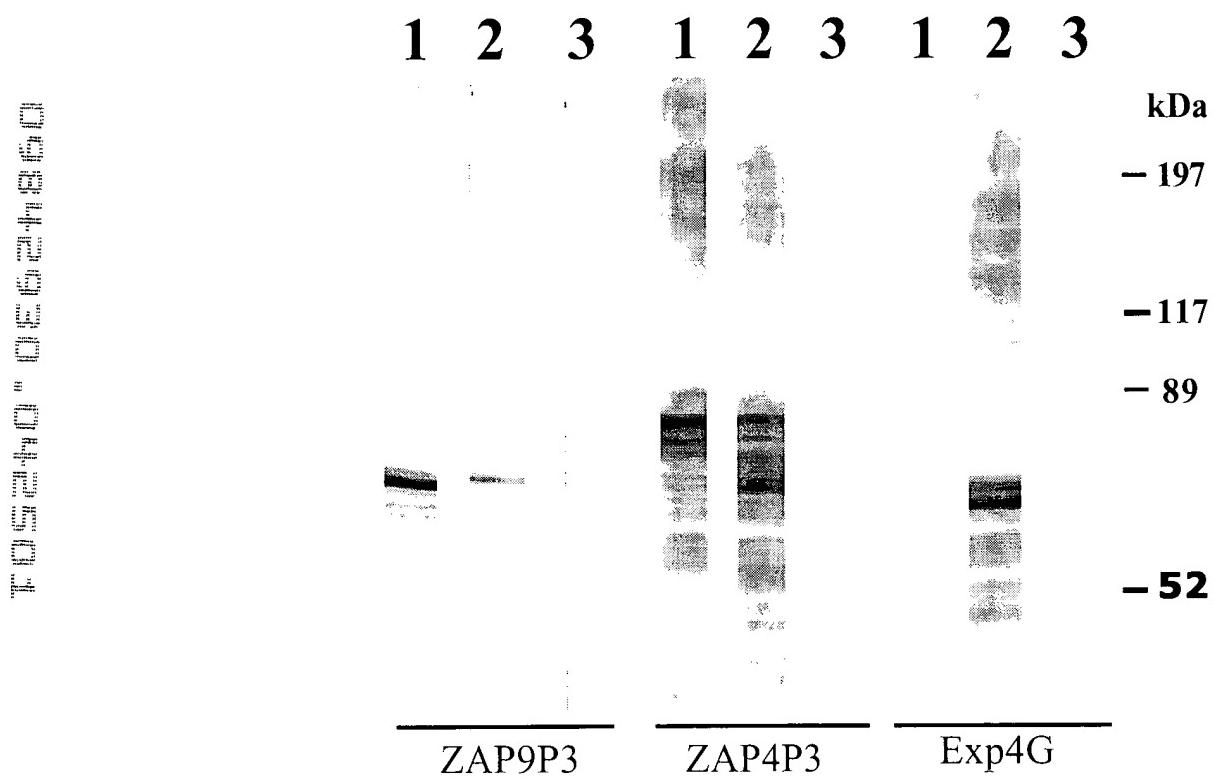


Figure 21

Figure 22

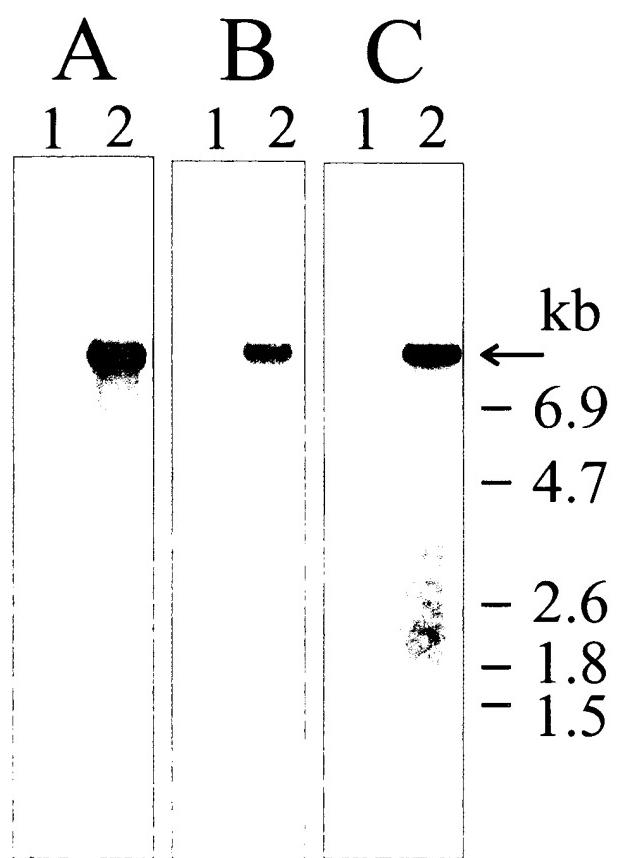
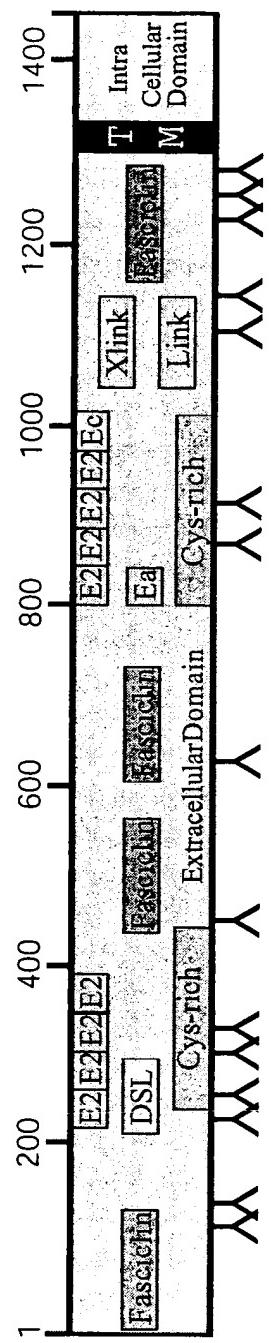


Figure 23



Ig kappa chain Leader Sequence

Figure 24

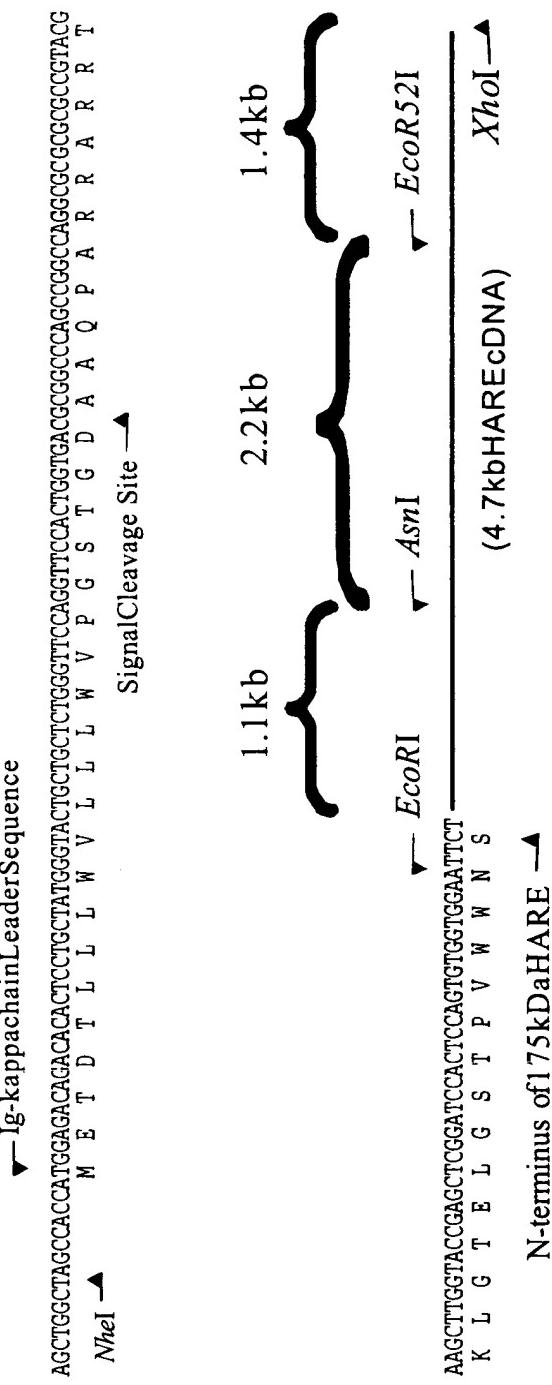
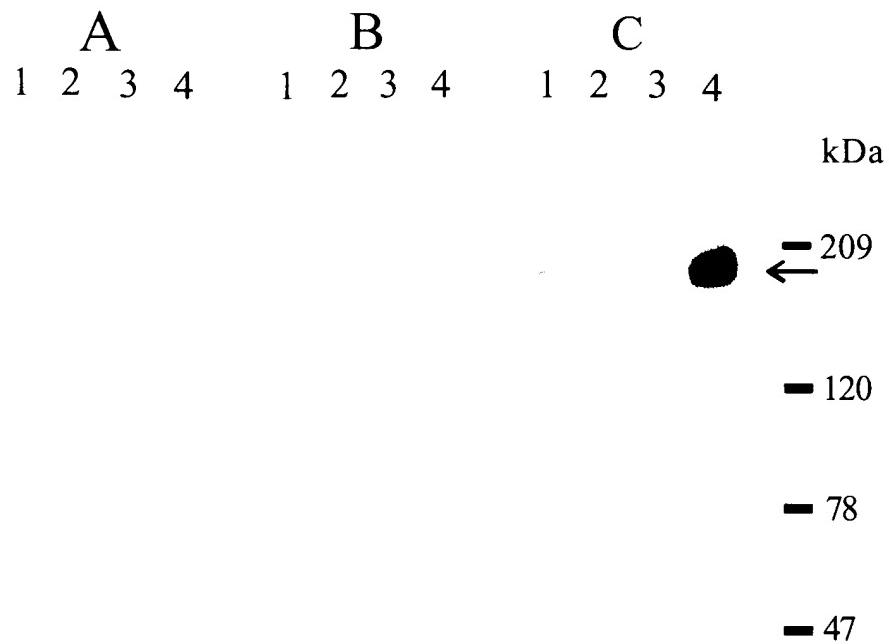


Figure 25

Autoradiography



Western Blot

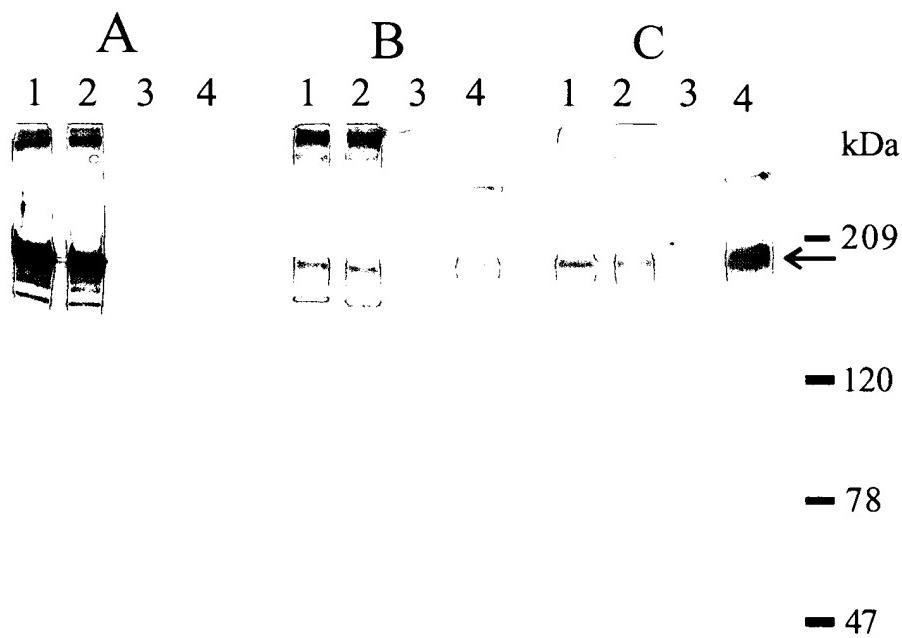


Figure 26

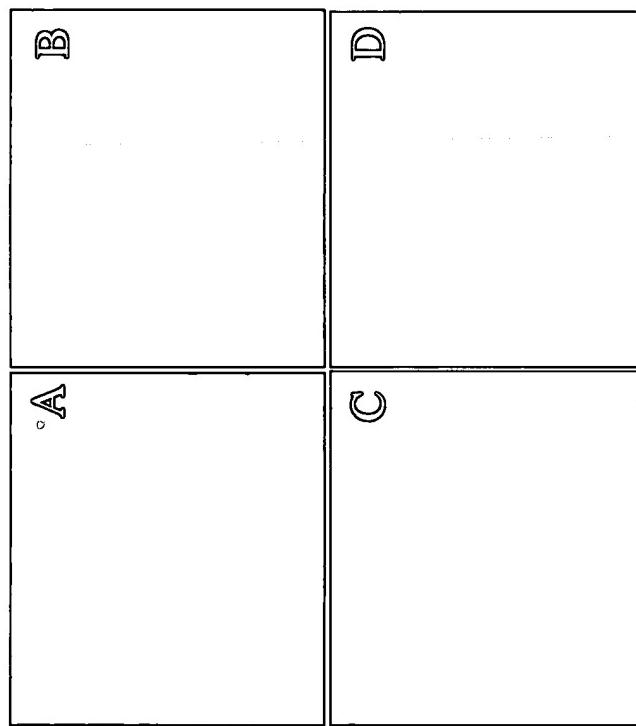


Figure 27A

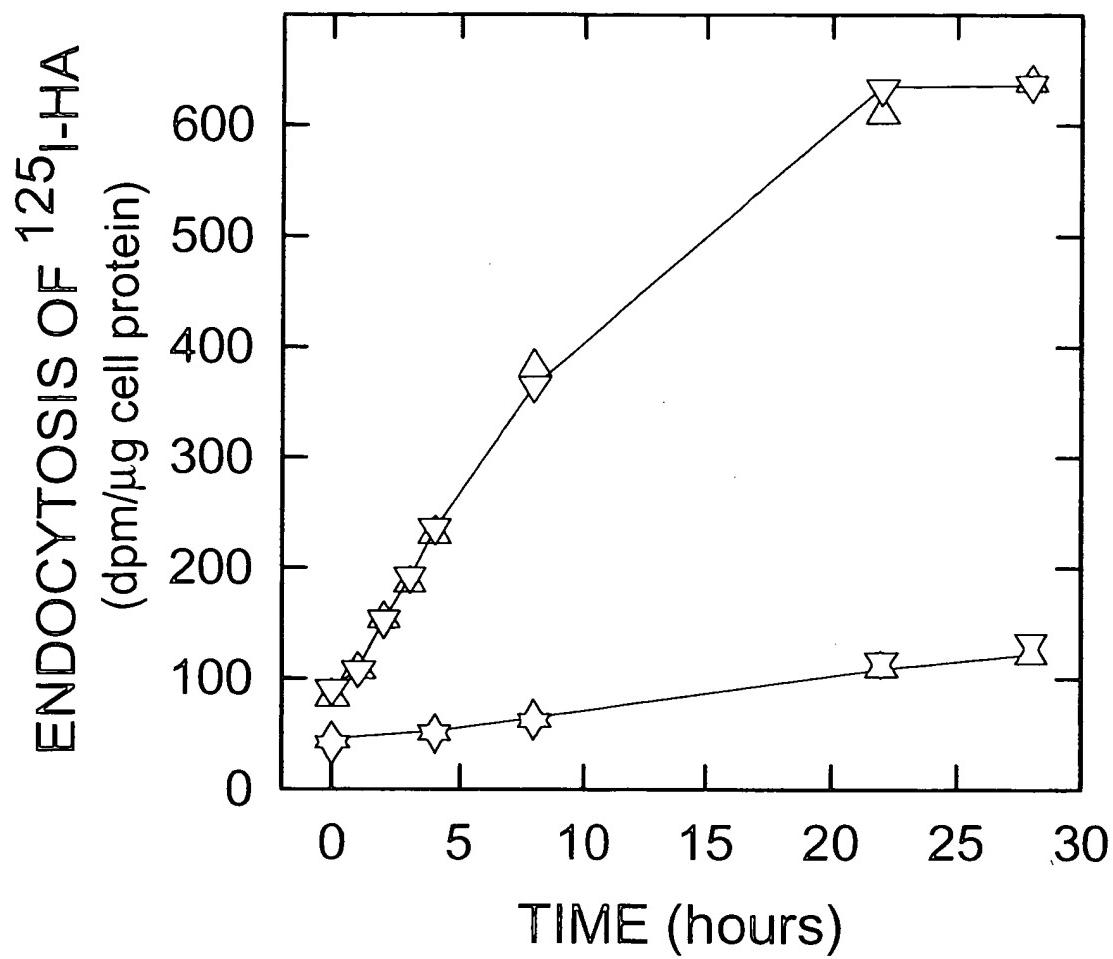


Figure 27B

Degradation of internalized HA by transfected SK-Hep1 cell lines expressing the 175-kDa HARE

Transfected Cells

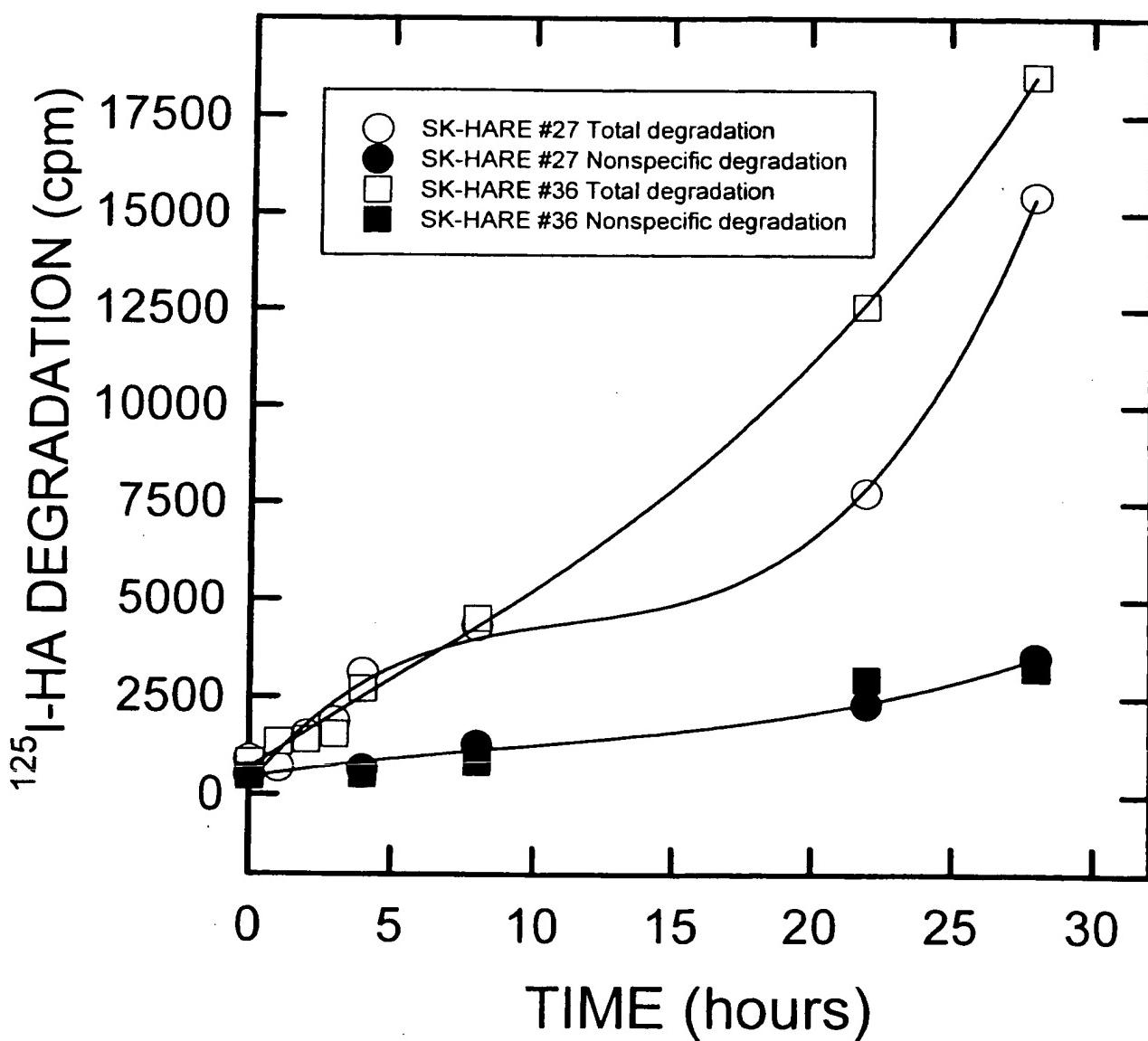


Figure 27C

Hyperosmolarity inhibits HA endocytosis mediated by HARE in transfected SK-Hep1 cells

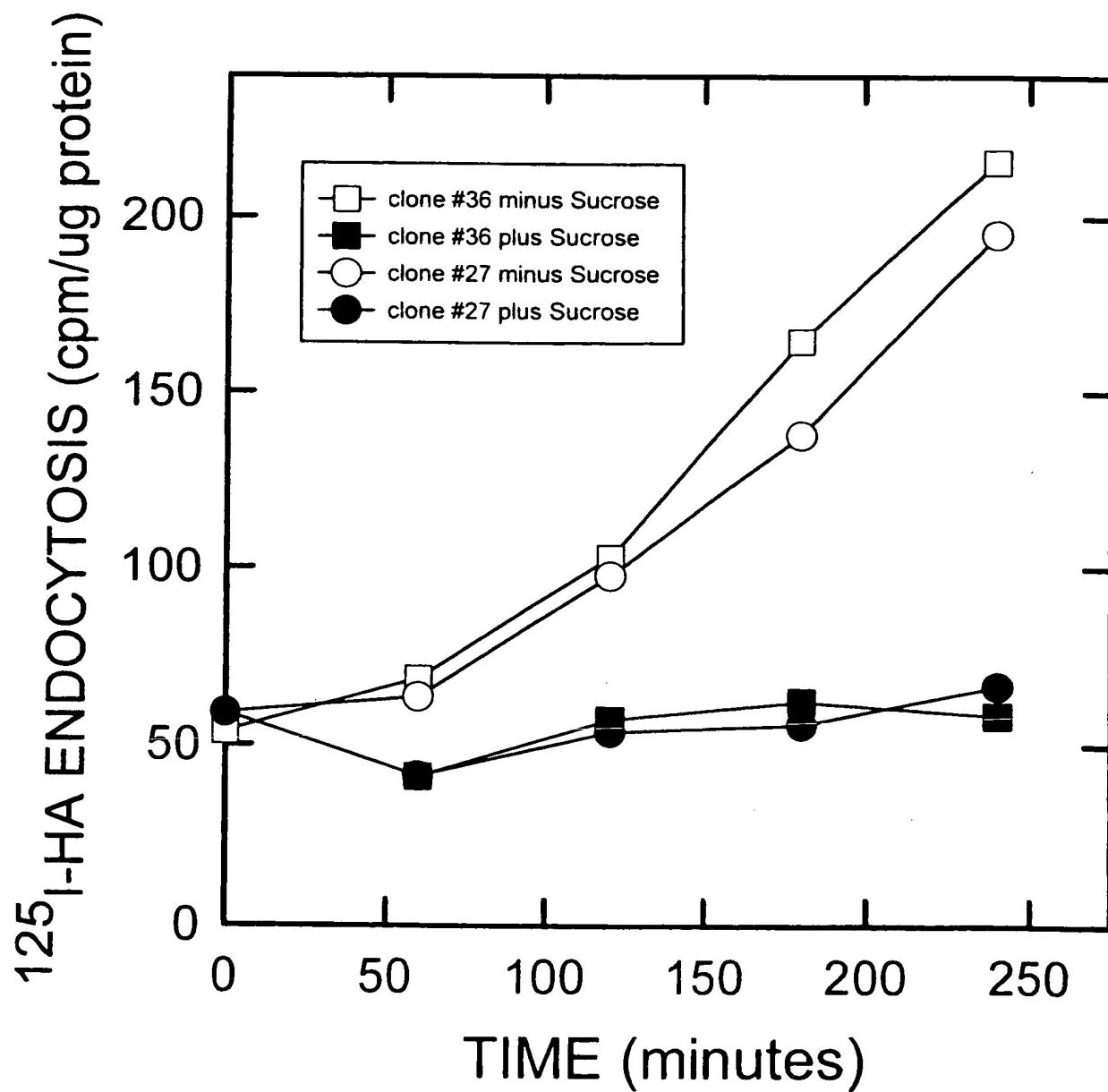


Figure 27D

Specific monoclonal antibodies against HARE inhibit HA endocytosis in SK-Hep1 transfectants expressing the 175-kDa HARE

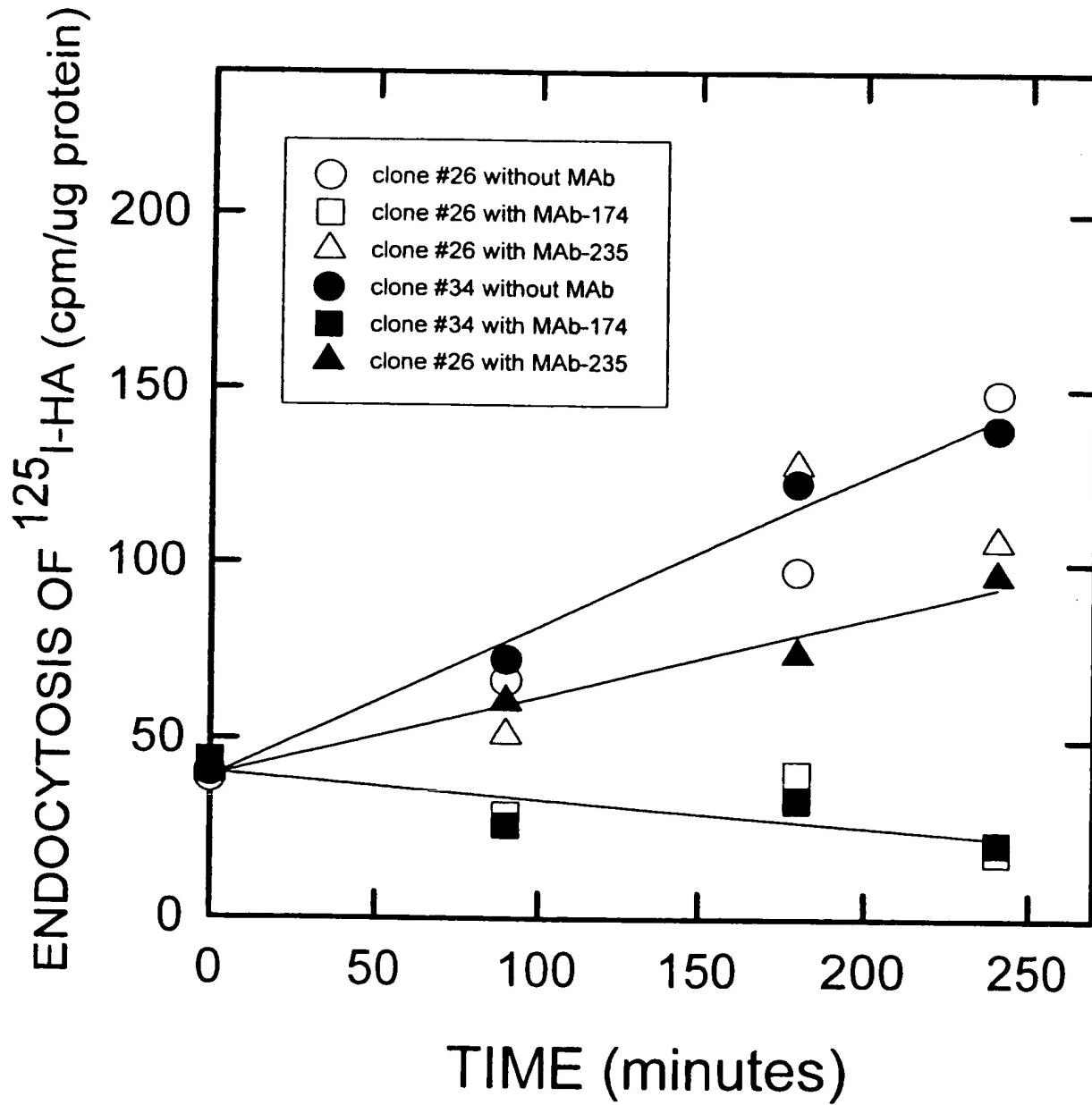


Figure 28

175HARE 1 ----- SLPS LLTRLBEQMPD YSIFRGIYIHH YNLASAIESA DAYTIVFVPPN EAIENYIREK KATSILKEDIL RYHVVLGKEL LKNDLHNGMH RETMLGFSVL
 CAB61827 1111 LHILSQVLLP PRGDVPGQQ LLQQLDLVPA FSLFRELLQH HGLVPQIEAA TAYTIVFVPTN RSLEA---QG NSSHLADATV RHHVVLGEAL SMETLRKGHH RNSSLGPASH
 BAA13377 754 LHILSQVLLP PRGDVPGQQ LLQQLDLV-A FSLFRELLQH HGLVPQIEAA TAYTIVFVPTN RSLEA---QG NSSHLADATV RHHVVLGEAL SMETLRKGHH RNSSLGPASH

175HARE 95 LAFFRLNDQL YVNEAPINYT NVATDKVIIH GLEKVLEIHK NRCDNNNTII VRGEQGKCSQ QAPQPLETKP LRETRK-CIY SIYFMGKRSV FIGCOPQCRV TIITRAONLA
 CAB61827 1218 IVFYNHSCQP EVNHVPLEGP MLEAPGRSLI GLSGVLTVG SRLCHSHAE A LREKCVNGTR RFRCTQGQFL QDTPRKSCVY RSGPSFSR-- GCSYTCAK KIQVPLCCPG
 BAA13377 861 IVFYNHSCQP EVNHVPLEGP MLEAPGRSLI GLSGVLTVG SRLCHSHAE A LREKCVNGTR RFRCTQGQFL QDTPRKSCVY RSGPSFSR-- GCSYTCAK KIQVPLCCPG

175HARE 204 SLAHNAK PAP GEVK-MQALG TASVWDGVN TGTGCGGLGF NGTAESETTE GKYGIRHDDQA DSCVHGRQSQ GPLGDSGCD DVGWRGVKCD MEITTDDNCNG TCHTSANGL
 CAB615793 1 ----- W HLFWS---DG TGVGCGEGF STCAESETTE GKYGIRHDDQA DSCVHGRQSQ GPLGDSGCD DVGWRGVKCD NATTEDNCNG TCHTSANGL
 CAB61358 1 -----
 CAB61827 1224 FFGTLCPCP GGLGGVGS-G HGQCQDRFLG SGECHCHEGF HGTACEVDEL GRYGPNCITGV DDCAGLICQE GLOGDGSVCV NVGWQGLRQD QKITSPOCPR KCDPNANGVQ
 BAA13377 967 FFGTLCPCP GGLGGVGS-G HGQCQDRFLG SGECHCHEGF HGTACEVDEL GRYGPNCITGV DDCAGLICQE GLOGDGSVCV NVGWQGLRQD QKITSPOCPR KCDPNANGVQ

175HARE 313 DPDGKASCKC AAGFRGNGTV CTAIAEIS NGGCSAKADQ KRTPGCRVRC VCKAGYTDG IVCLIEINPL ENHGCDKNA ECTQTGPQNA VENCLPKYT DG-KVCLIN
 BAB615793 90 NSDGTASCKC AAGFQNGTI CTAIAEIS NGGCSAKADQ KRTPGCRVRC VCKAGYTDG IVCLIEINPL ENHGCDKNA ECTQTGPQNA ACNCLPAYTG DG-KVCLIN
 CAB61358 3 EAVGTASCKC AAGFQNGTI CTAIAEIS NGGCSAKADQ KRTPGCRVRC VCKAGYTDG IVCLIEINPL ENHGCDKNA ECTQTGPQNA ACNCLPAYTG DG-KVCLIN
 CAB61827 1433 DSAGASTQAC AAGYSGNGII CSEVDPQAHG HGCGSPHANC TKVAPQGRTQ TCQDGYMDG ELQOEINSCL IHGGCHIHA ECIPTGPQOV SISCREGYSG DGIRTCELLD
 BAA13377 1076 DSAGASTQAC AAGYSGNGII CSEVDPQAHG HGCGSPHANC TKVAPQGRTQ TCQDGYMDG ELQOEINSCL IHGGCHIHA ECIPTGPQOV SISCREGYSG DGIRTCELLD

175HARE 422 VCLTNNGGCS PFAFCNQYTEQ DORICICKP Y-TGDDIVER GSIFYELPKN PSTSQYFFQ PDEAHVERLAG PGPFPTVFPAP -- LSSSFNHE PRIKDJDQOG LMSQVLRHYV
 BAB615793 199 VCLTNNGGCS EFAICNHTGQ VERTCICKPN Y-IDGDFTR GSIFYELPKN PSTSQYFFQ QEFVFKDLVG PGPFPTVFPAP -- LSAAPDEE ARVKDWDKVG LMSQVLRHYV
 CAB61358 112 VCLTNNGGCS EFAICNHTGQ VERTCICKPN Y-IDGDFTR GSIFYELPKN PSTSQYFFQ QEFVFKDLVG PGPFPTVFPAP -- LSAAPDEE ARVKDWDKVG LMSQVLRHYV
 AAF82398 1 -----
 CAB61827 1543 PCSKNNGGCS PYATKSTGD QRFTCQDTA HTVGDGLTER ARVGLELLRD KHAS--FFSL RLLEYKELKG DGPFTIFVPH ADLMSNLSQD ELARIRAHQ L--VFRYHV
 BAA13377 1186 PCSKNNGGCS PYATKSTGD QRFTCQDTA HTVGDGLTER ARVGLELLRD KHAS--FFSL RLLEYKELKG DGPFTIFVPH ADLMSNLSQD ELARIRAHQ L--VFRYHV

175HARE 528 VGCOQLLEN LKVITTSATT QGEPVISVS QDTPVFINNEA KVLSDDIIIST NGVIVHIDKL LSPKNLLITP KDALGRVLQN LTIVAAHNG TKFSKLQDS GLLSVITDSI
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 BAA13377 1291 VGCRRLRSED LLEQYATAL SGHPLRFSE EGSIYLNDFA RVVSSDHEAV NGILHFIDRV LLPPEALHWE PDDAPIPRRN VTAAGQFGV KIFSGLLKVA GLLPLLREAS

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 BAA13377 1401 HRPTFLWPT DAAFRALPPD RQAWLYHEDH RDKLAAILRG HMIRNEALA SDLPNLGPL TMHGTPISFS CSRTRP-GEL MVGEDDARIV QRLHPFEGGL AYGIDQLEP

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 AAF82398 230 PTLGGRCDTF TFTDAS-GEC GSQVNTPSCP RWSXPKGVKQ KC---LY-----N-LPP K-----RNLE-GC RECRSLVIIQI PROCHGYPGR DCQACPGGP
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175HARE 833 TPCNNRGMCR DLYTPMGQCL CHTGFGNTA ELCWHGRFGP DQQRPSCESEH GQCDDEGIFTG GCLCETGWT AASCIDTPAV FAVCTPACSV HATCKENNTIC VCNLYEGDG
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175HARE 1162 CTOKAGYVGD GFS-EISGNLL QVLMSPFSLT NFLTEVLA FS KSSARGOFL KHLTDLISR TLFPVQNSGL PGNSLSLGRD IEHHLTNVNV SFYNDLVNGT FLRIMLGSOL
 BAB615793 938 CTCKVGYVGD GFS-EISGNLL QVLMSPFSLT NFLTEVLA FS NSSARGAFL EHLTDLISR TLFPVQNSGL GENETLSSRD IEHHHLANVSM FFYNDLVNGT TLQTRLGSKL
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 AAF82398 643 CTCKVGYVGD GFS-EISGNLL QVLMSPFSLT NFLTEVLA FS NSSARGAFL EHLTDLISR TLFPVQNSGL GENETLSSRD IEHHHLANVSM FFYNDLVNGT TLQTRLGSKL
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175HARE 1271 LITFS-QD QLHQ-ETRFV DGRSILQWDI IAANGLHII SEPLRAPPATA ATA---AHSG LGTGFCAV LVTGAI---L AJAYSYFRIKQ RTIG--FQRF DQKRTLMSWL
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 BAA13377 2166 SPWQ-EGTN- PTLVSPNVP FGSDTCEPF DD-----SLLEEDFPD TORILITVK----

Figure 29

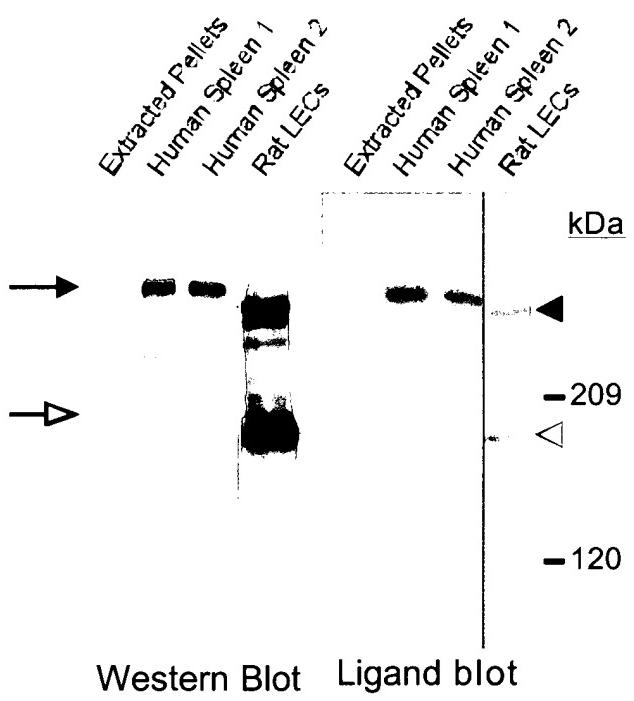


Figure 3 0

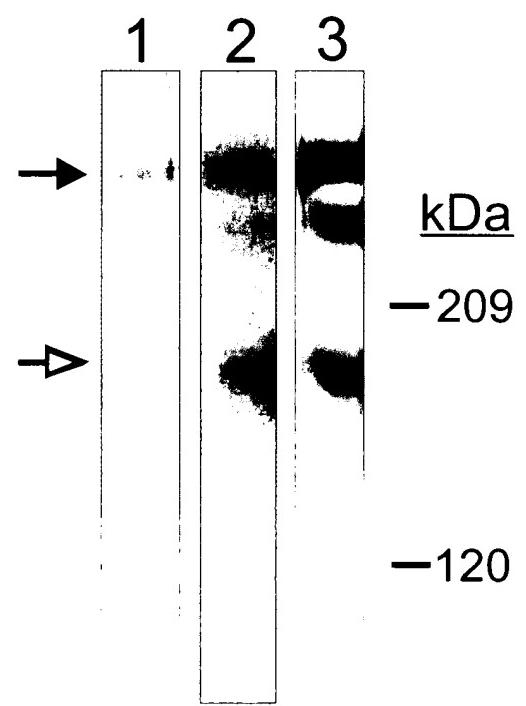


Figure 31

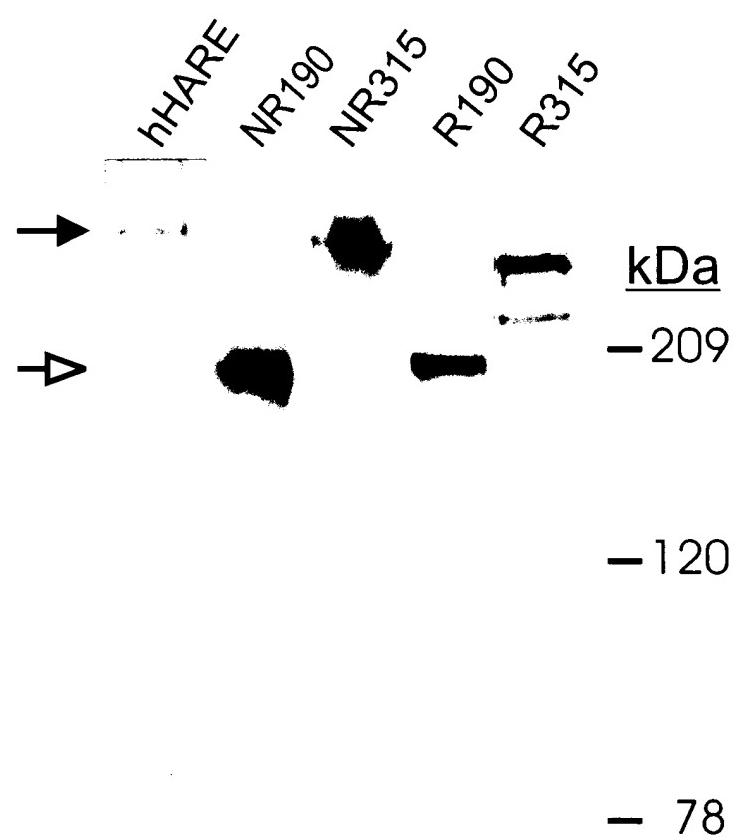
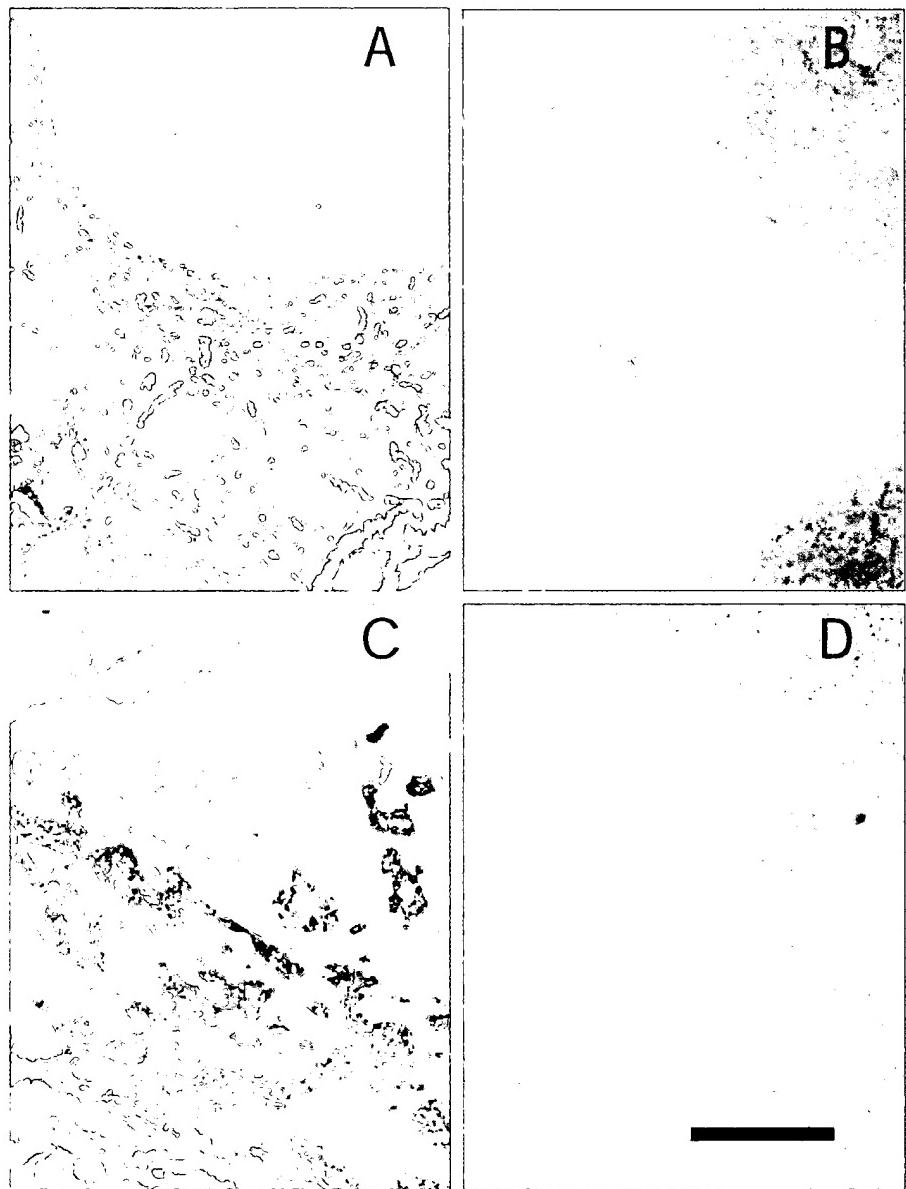


Figure 3 2



TO 2010 "05247650

Figure 33

Figure 34

Figure 34

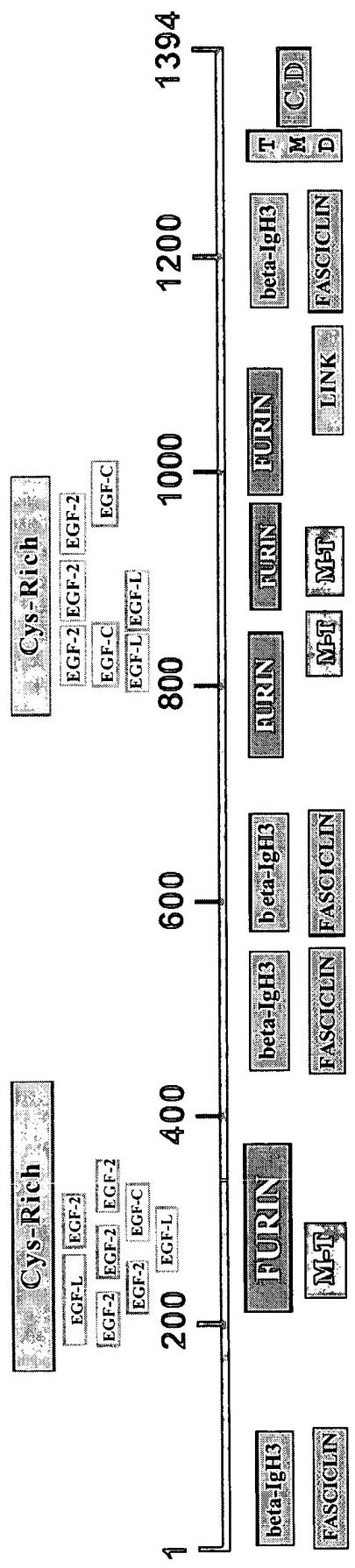


Figure 35

| | | | |
|----------------|-----------|--|---|
| hHARE rHARE | 1 23 | I OYNLANAEAADAYTVFAP NNEAIENYIREKKVLSLEED VLRYHVLLEKLLRNDLHNG MRETMLGFSYFLHND MRETMLGFSYLLAFLRND QLYVNNEAPINTNVA | |
| hHARE rHARE | 101 123 | I HGLGKVLEIQQKR DNNDDT TIRGRRT SSELTPFGT KSLGNEKRR YTSYFMGRR TLFIG QPKIVRTVTIRE SVFIG QPQIVRTIITRAW LASLAHNAPAPEVKMCAL | |
| hHARE rHARE | 201 222 | GNGICLDGVANGTGV E GEG FSGTA ET TEGKYGIH DQ A S VHGR INGPLGDGSID DVGWRGVH DNATTEDN GT HTSAN LTNS DGTAS K | A S VHGR SQGPLGDGSID DVGWRGVH DMETTDN GT HTSAN LLDPDGKAS K |
| hHARE rHARE | 301 322 | [AAGFOGNGTII TAINA EI SNGG SAKAD KRTTPGRRV T KAGYTGDGIV LEINP LENHGG DNAE TQTPGNO AA N ILPAYTGDKV TLIN | V KAGYTGDGIV LEINP LENHGG DNAE TQTPGNO AV N LPKYTGDKV SLIN |
| hHARE rHARE | 401 422 | V LTNNGG SEPAINTT Q VERTT KPNYXGDGFT RG SIYOELPKNPKTSQYFFOLQ EH芙VLDYGPFTVAPLS AADEFEEARVKDWDKYGLMPQ | V LTNNGG SPFAF NYT Q DQRIT KPDYTGDGIV RG SIYGEPLPKNPSTSQYFFQLQ EHAVRELAGPGPFTVAPLS SSFNHEPRIKDWDQQGLMSQ |
| hHARE rHARE | 501 522 | VLRYHVV A HOLLLENKLII SNATSLOQEPIVISVSQSTV YINNKAKI ISSDI LISTNGIV H1DCKLSPKNLLITPKDNS GRILQMLTTLATNGYIKFS | VLRYHVV QQLLDNLKVT TSATTLOQEPEVSISSQDTV FINNEAKVLSDDI LISTNGVI H1DCKLSPKNLLITPKDAL GRLQMLTTVAANGYTKFS |
| hHARE rHARE | 601 622 | NLIQDSGLLSVITDPIHTPV TLFWPTDOALHALPAEQODF LFNODNNDKDLKEYLKFKHVR DAKVLAVIDLPTSTAWKTLQG SELSVKT GAGRDI | NLIQDSGLLSVITDSIHTPV TVFWPTDKALEALPPEQQDF LFNQDNNDKDLKSYLKFKHVR DSKALASDLPRSAWSWKTQG SELSVR GTGSDIGELFLNE |
| hHARE rHARE | 701 722 | QTTRIVORELIFDLGYAYGI DILLIDPTLGCR DTFITFD ASGE GSIVNTPS PRWSKP KGVKKK LYN LPFKRNLEG RER SLVQI PR | 701 QTTRIVORELIFDLGYAYGI DILLIDPTLGCR DTFITFD IPGETPSK KGVKKK LYN LPFKRNLEG RER SLVQI PR |
| hHARE rHARE | 800 822 | RD OA PGGDAP NNRCV LDQYSATGET K INTGFNGTA JEM WPGRFGPD LPCCG ISD HQO DDDGITGSGQL ETGW TGPSIDTOAVLP | RD OA PGGDAP NNRCV RDLYTPMGQ L HTGFNGTA JEL WHGRFGPD QPSR SE HQO DEGIGSGE L ETGW TAAS DPTPAVFAVTPAIS |
| hHARE rHARE | 900 922 | AHAT KENTT ENLDYEGD GIT TVVDF KQDNGG JAKV AR SQKGTVS S QKGYKG DGHS TEIDP ADGLNGG EHAT KMTGPCKHM E KSH | AHAT KENTT ENLDYEGD GIT TVVDF KQNNGG JAKV AK SQKGTVS S KKGYKG DGYS TEIDP ADGVNGG EHAT RMTGPCKHM E KSH |
| hHAR rHARE | 1000 1022 | YVGDLN JEP EQOLPDR LQ DNGQ HADAK VDLHFQDTT VGVEHLLRSPLGQYKLTFDKA REA ANEAATMAYNOLSYA OKAYHL | YVGDLN JEP EQOLPDR LQ DNGQ HPDAS ADLYFQDTT VGVEHLLRSPLGQYKLTFDKA KEA AKEATIATYNOLSYA OKAYHL |
| hHARE rHARE | 1100 1122 | P TAFASON GSGVVGIVDYG PRPNK SEMWDF YRMKDVN T KVGYVGDF S GNLQ VMSFPSLTNFLETEVLAYSN SSARGAPLEHLTDLSIRGT | P TAFASON GSGVVGIVDYG PRPNK SEMWDF YRMKDVN T KVGYVGDF S GNLQ VMSFPSLTNFLETEVLAFSK SSARGAFLKHLTDLSIRGT |
| hHARE rHARE | 1200 1222 | LFPQNQNSGLGENETLSGRDI EHHIANVSMFYNDLVNGT LQTRLGSKLLITASQDPLQP TETRFVDGRAILQWDIFASN GIIHVISRPLKAPPAPVUTLT | LFPQNQNSGLPGNKSLSGRDI EHHLTNVNVSFYNDLVNGT LRTMLGSQLLITFSQDQHQ -ETRFVDGRSLQWDIIAN GILHISSEPLRAPTAATAA |
| hHARE rHARE | 1300 1321 | HTGLGAGI FAIIILVTGAVA LAAYSYFR INRTIG QHFE SEEDINVAALGKQOPENISN PLTESTESAPPESP DPFID SEEROLEGNDPLRLT | HTGLGAGI FAIIILVTGAVA LAAYSYFR KQRTGQRF QKRTLMSWLASSSPRI SQC LCMRPOQRHPOSQ PPVPSQ LENRIWRTA LWGHCGPDMR |
| hHARE | 1421 | SQQATTVTVPR | → |

Figure 36

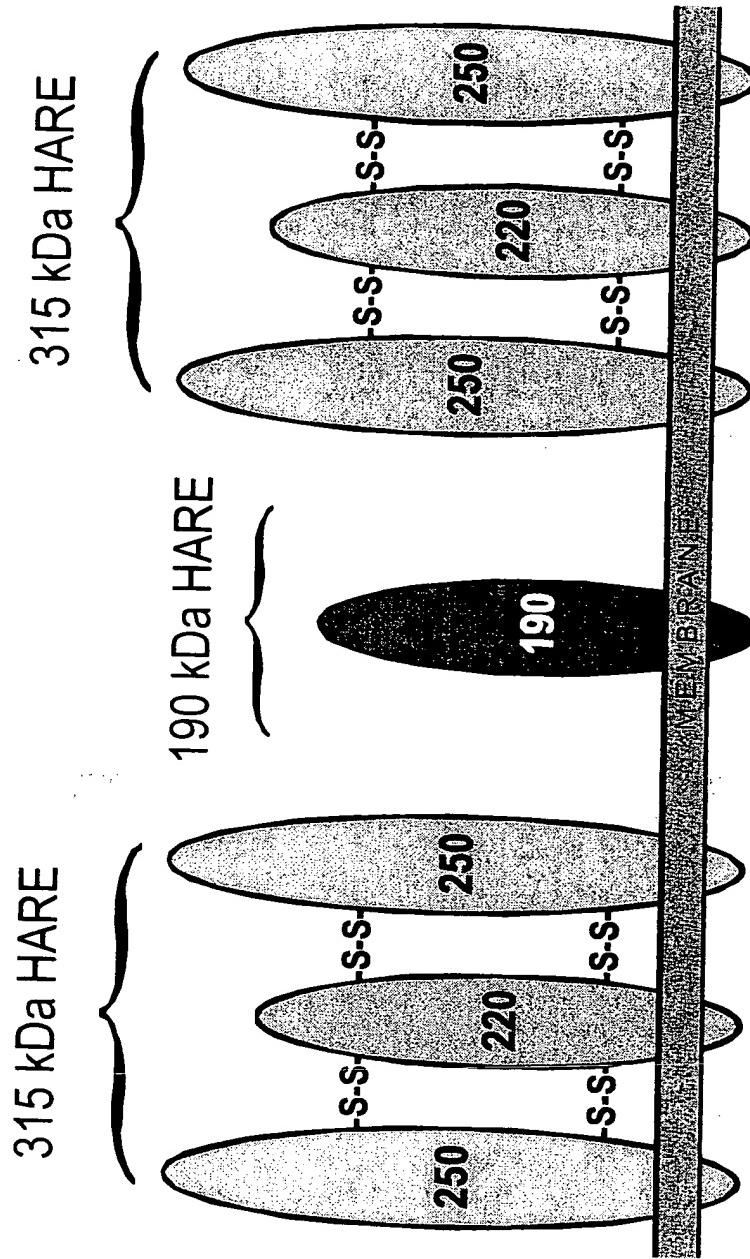


Figure 37

Amplification of the 1394 amino acid HARE
Open Reading Frame from a human lymph
node cDNA Library

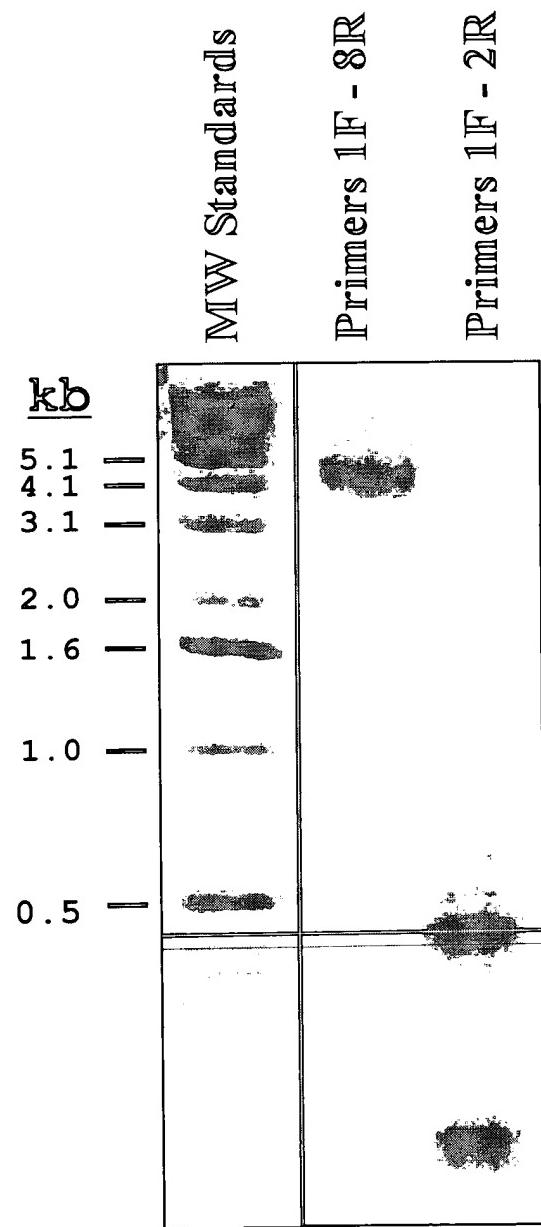


Figure 38

Schematic Organization of the Human HARE Gene on Chromosome 12
(encoding 1357 of the 1394 amino acids disclosed here)

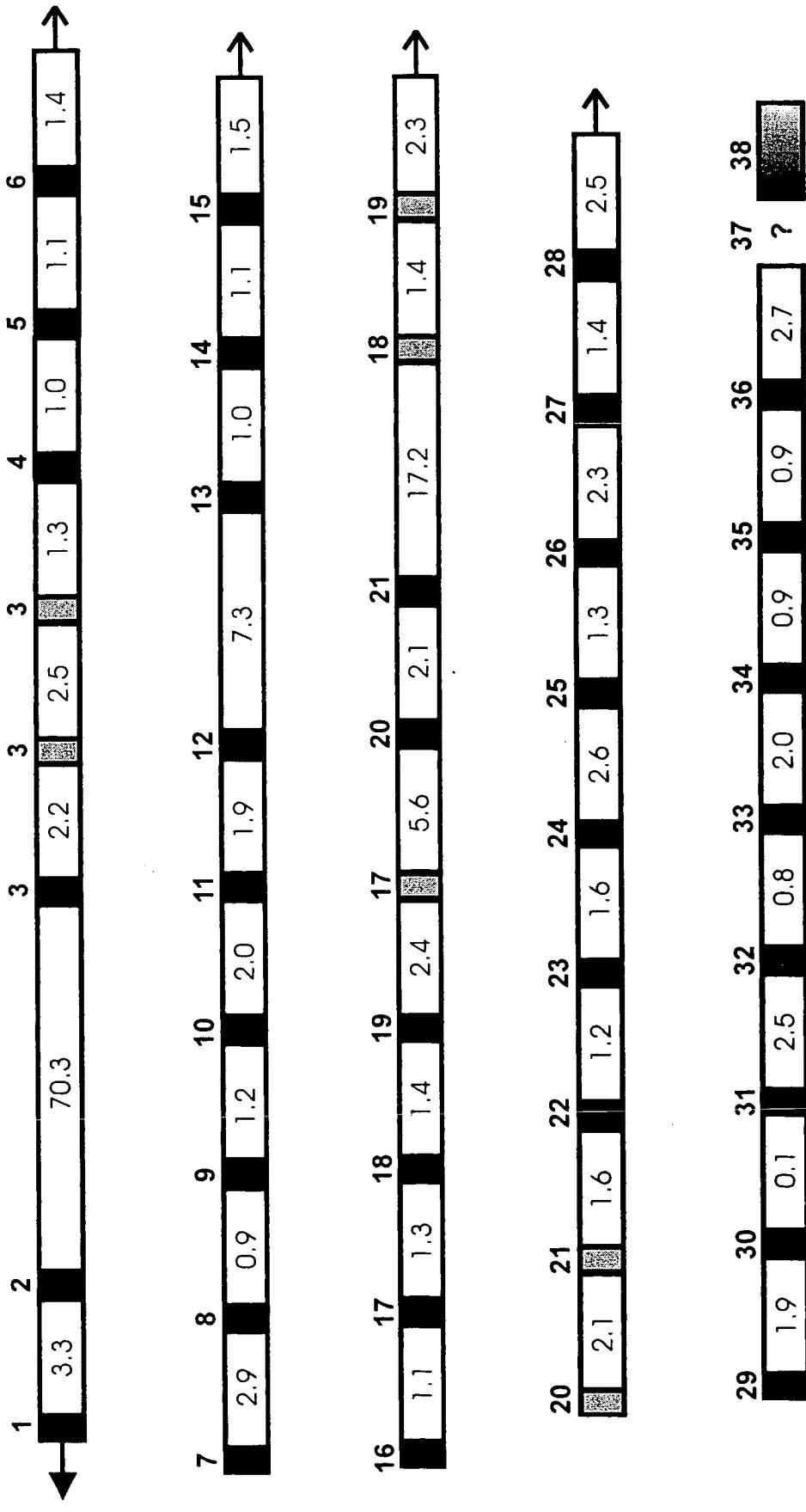


Figure 3 9

